

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1785

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>

<221> CDS

<222> (1)..(1785)

<220>

<221> N\_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

<400> 1

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1				5				10					15			

ggt	tcc	act	ggt	gac	tct	aga	atg	gtc	cag	gcc	tcg	atg	agg	agc	cca	96
Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	
			20					25				30				

aat	atg	gag	acg	ttc	aaa	cag	cag	aag	gtg	gag	gac	ttt	tat	gat	att	144
Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	
		35				40					45					

gga	gag	gag	ctg	ggc	agt	ggc	cag	ttt	gcc	atc	gtg	aag	aag	tgc	cgg	192
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	
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gag	aag	agc	acg	ggg	ctg	gag	tat	gca	gcc	aag	ttc	att	aag	aag	agg	240
Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	
65					70					75					80	
cag	agc	cgg	gcc	agc	cgt	cgg	ggc	gtg	tgc	cgg	gag	gaa	atc	gag	cgg	288
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	
				85					90						95	
gag	gtg	agc	atc	ctg	cgg	cag	gtg	ctg	cac	ccc	aac	atc	atc	acg	ctg	336
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	
			100					105						110		
cac	gac	gtc	tat	gag	aac	cgc	acc	gac	gtg	gtg	ctc	atc	ctt	gag	cta	384
His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	
		115					120					125				
gtg	tcc	gga	gga	gaa	ctg	ttt	gat	ttc	ctg	gcc	cag	aag	gag	tcg	tta	432
Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu	
	130					135					140					
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Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val	
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aat	tac	ctt	cac	aca	aag	aaa	att	gct	cac	ttt	gat	ctc	aag	cca	gaa	528
Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	
				165					170						175	
aac	atc	atg	ttg	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	576
Asn	Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu	
			180					185					190			
att	gac	ttt	ggc	ctg	gct	cac	gaa	ata	gaa	gat	gga	gtt	gaa	ttt	aaa	624
Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	
		195					200					205				
aac	att	ttt	ggg	aca	cct	gaa	ttt	gtt	gct	cca	gaa	atc	gtg	aac	tat	672
Asn	Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	
	210					215					220					
gag	cca	ctg	gga	ctg	gag	gcc	gac	atg	tgg	agc	att	gga	gtc	atc	acc	720
Glu	Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	
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tat	atc	ctt	cta	agt	gga	gcg	tcc	ccc	ttc	ctg	gga	gac	aca	aaa	caa	768
Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	
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gaa	acc	ctg	gca	aat	atc	act	gct	gtg	agt	tac	gac	ttt	gat	gag	gaa	816
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	
			260					265					270			
ttc	ttc	agc	cag	aca	agc	gag	ctg	gcc	aag	gac	ttc	att	cgg	aag	ctt	864
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	
		275					280					285				

ctt	gtg	aaa	gag	acc	cgg	aaa	cgg	ctt	acc	atc	caa	gag	gct	ctc	aga	912
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	
	290						295					300				
cat	ccc	tgg	atc	gga	tcc	aaa	cta	gct	gag	cac	gaa	ggg	gac	gcg	gcc	960
His	Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Gly	Asp	Ala	Ala	
	305					310				315					320	
cag	ccg	gcc	atg	gcc	cag	gtc	aag	ctg	cag	gag	tca	ggg	act	gaa	ctg	1008
Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu	
				325					330					335		
gca	aag	cct	ggg	gcc	gca	gtg	aag	atg	tcc	tgc	aag	gct	tct	ggc	tac	1056
Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	
			340					345					350			
acc	ttt	act	gac	tac	tgg	atg	cac	tgg	gtt	aaa	cag	agg	cct	gga	cag	1104
Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	
		355					360					365				
ggg	ctg	gaa	tgg	att	gga	tac	att	aat	cct	aac	act	gct	tat	act	gac	1152
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	Thr	Asp	
	370					375					380					
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Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	
	385				390					395					400	
tcc	agc	aca	gcc	tac	atg	caa	ctg	cgc	agc	ctg	acc	tct	gag	gat	tct	1248
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	
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gca	gtc	tat	tac	tgt	gca	aaa	aag	aca	act	cag	act	acg	tgg	ggg	ttt	1296
Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp	Gly	Phe	
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cct	ttt	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	gga	ggc	1344
Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
		435					440					445				
ggg	tca	ggc	gga	ggg	ggc	tct	ggc	ggg	ggc	gga	tgc	gac	att	gtg	ctg	1392
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Leu	
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Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	Val	Thr	
	465				470					475					480	
ttg	agc	tgc	aag	gcc	agt	gag	aat	gtg	gat	tct	ttt	gtt	tcc	tgg	tat	1488
Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	Trp	Tyr	
			485					490						495		
caa	cag	aaa	cca	ggc	cag	tct	cct	aaa	ctg	ctg	ata	tac	ggg	gcc	tcc	1536
Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	
			500					505					510			

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Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly	
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aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac ctt gca	1632
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala	
530 535 540	
gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc ggt gct	1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala	
545 550 555 560	
ggc acc aag ctg gaa atc aaa cgg gcg gcc gca ggg ccc gaa caa aaa	1728
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Gly Pro Glu Gln Lys	
565 570 575	
ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat	1776
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His His	
595	

<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2

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Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile	
35 40 45	
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg	
50 55 60	
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
65 70 75 80	
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu	
115 120 125	
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu	
130 135 140	
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val	
145 150 155 160	
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu	
165 170 175	
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu	

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<211> 1794

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:

pMS-(Ki-4-DAPK2')-II/G ORF

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<222> (1)..(1794)

<220>

<221> N\_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

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1 5 10 15	
ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg	96
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu	
20 25 30	
cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg	144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met	
35 40 45	
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg	192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp	
50 55 60	
gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat	240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	
65 70 75 80	
cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc	288
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
85 90 95	
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca	384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
115 120 125	
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc	432
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val	
130 135 140	
acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt	480
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	

145		150		155		160	
ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg	528						
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met							
		165		170		175	
tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg	576						
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val							
		180		185		190	
gat tct ttt gtt tcc tgg tat caa cag aaa cca gcc cag tct cct aaa	624						
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys							
		195		200		205	
ctg ctg ata tac ggg gcc tcc aac cgg tac act ggg gtc ccc gat cgc	672						
Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg							
		210		215		220	
ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt	720						
Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser							
		225		230		235	
gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag aat tac agg	768						
Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg							
		245		250		255	
tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg	816						
Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala							
		260		265		270	
gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat	864						
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn							
		275		280		285	
atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga	912						
Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly							
		290		295		300	
gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag	960						
Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu							
		305		310		315	
aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg cag	1008						
Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln							
		325		330		335	
agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg gag	1056						
Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu							
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gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg cac	1104						
Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His							
		355		360		365	
gac ctc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta gtg	1152						
Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val							

370	375	380	
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Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser			
385	390	395	400
gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg aat			1248
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn			
	405	410	415
tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac			1296
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn			
	420	425	430
atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg att			1344
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile			
	435	440	445
gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa aac			1392
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn			
	450	455	460
att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat gag			1440
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu			
	465	470	480
cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat			1488
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr			
	485	490	495
atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa gaa			1536
Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu			
	500	505	510
acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc			1584
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe			
	515	520	525
ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt ctt			1632
Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu			
	530	535	540
gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga cat			1680
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His			
	545	550	560
ccc tgg atc gga tcc aaa cta gct gag cac gaa ttt cga gga ggg ccc			1728
Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro			
	565	570	575
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat			1776
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His			
	580	585	590
cat cat cat cat cat tga			1794
His His His His His			



595

<210> 4  
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 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence:  
 pMS-(Ki-4-DAPK2')-II/G ORF

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 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met  
 35 40 45  
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp  
 50 55 60  
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn  
 65 70 75 80  
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala  
 85 90 95  
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg  
 100 105 110  
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr  
 115 120 125  
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val  
 130 135 140  
 Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
 145 150 155 160  
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met  
 165 170 175  
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val  
 180 185 190  
 Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 195 200 205  
 Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg  
 210 215 220  
 Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser  
 225 230 235 240  
 Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg  
 245 250 255  
 Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala  
 260 265 270  
 Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn  
 275 280 285  
 Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly  
 290 295 300  
 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu  
 305 310 315 320  
 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln  
 325 330 335  
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<210> 5
<211> 3102
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: pMT-Ki-4  
(scFv)-eEF-2K ORF

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<223> pelB leader sequence
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1 5 10 15

gcc Ala	cag Gln	ccg Pro	gcg Ala 20	atg Met	gcc Ala	atg Met	ggc Gly	cat His 25	cat His	cat His	cat His	cat His 30	cat His	cat His	cat His	96
cat His	cac His	agc Ser 35	agc Ser	ggc Gly	cat His	atc Ile	gac Asp 40	gac Asp	gac Asp	gac Asp	aag Lys	cat His 45	atg Met	aag Lys	ctt Leu	144
atg Met	gcc Ala 50	cag Gln	ccg Pro	gcc Ala	atg Met	gcc Ala 55	cag Gln	gtc Val	aag Lys	ctg Leu	cag Gln 60	gag Glu	tca Ser	ggg Gly	act Thr	192
gaa Glu 65	ctg Leu	gca Ala	aag Lys	cct Pro	ggg Gly 70	gcc Ala	gca Ala	gtg Val	aag Lys	atg Met 75	tcc Ser	tgc Cys	aag Lys	gct Ala	tct Ser 80	240
ggc Gly	tac Tyr	acc Thr	ttt Phe 85	act Thr	gac Asp	tac Tyr	tgg Trp	atg Met 90	cac His	tgg Trp	gtt Val	aaa Lys	cag Gln 95	agg Arg	cct Pro	288
gga Gly	cag Gln	ggc Gly	ctg Leu 100	gaa Glu	tgg Trp	att Ile	gga Gly	tac Tyr 105	att Ile	aat Asn	cct Pro	aac Asn 110	act Thr	gct Ala	tat Tyr	336
act Thr	gac Asp	tac Tyr 115	aat Asn	cag Gln	aaa Lys	ttc Phe	aag Lys 120	gac Asp	aag Lys	gcc Ala	aca Thr	ttg Leu 125	act Thr	gca Ala	gac Asp	384
aaa Lys	tcc Ser 130	tcc Ser	agc Ser	aca Thr	gcc Ala	tac Tyr 135	atg Met	caa Gln	ctg Leu	cgc Arg	agc Ser 140	ctg Leu	acc Thr	tct Ser	gag Glu	432
gat Asp 145	tct Ser	gca Ala	gtc Val	tat Tyr	tac Tyr 150	tgt Cys	gca Ala	aaa Lys	aag Lys	aca Thr 155	act Thr	cag Gln	act Thr	acg Thr	tgg Trp 160	480
ggg Gly	ttt Phe	cct Pro	ttt Phe 165	tgg Trp	ggc Gly	caa Gln	ggg Gly	acc Thr 170	acg Thr	gtc Val	acc Thr	gtc Val	tcc Ser 175	tca Ser	ggc Gly	528
gga Gly	ggc Gly	ggc Gly	tca Ser 180	ggc Gly	gga Gly	ggc Gly	ggc Gly	tct Ser 185	ggc Gly	ggc Gly	ggc Gly	gga Gly 190	tgc Ser	gac Asp	att Ile	576
gtg Val	ctg Leu	acc Thr 195	cag Gln	tct Ser	cca Pro	aaa Lys	tcc Ser 200	atg Met	gcc Ala	atg Met	tca Ser 205	gtc Val	gga Gly	gag Glu	agg Arg	624
gtc Val	acc Thr 210	ttg Leu	agc Ser	tgc Cys	aag Lys	gcc Ala 215	agt Ser	gag Glu	aat Asn	gtg Val	gat Asp 220	tct Ser	ttt Phe	gtt Val	tcc Ser	672
tgg Trp 225	tat Tyr	caa Gln	cag Gln	aaa Lys	cca Pro 230	ggc Gly	cag Gln	tct Ser	cct Pro	aaa Lys 235	ctg Leu	ctg Leu	ata Ile	tac Tyr	ggg Gly 240	720

gcc tcc aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly 245 250 255	768
tct gga aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp 260 265 270	816
ctt gca gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe 275 280 285	864
ggc gct ggc acc aag ctg gaa atc aaa cgg gcg gcc gca gag ctc ggc Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly 290 295 300	912
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gtt gat ggc ggc cag tcc ccc cga gct ggc cat gat ggt gat tct gat Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp 325 330 335	1008
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gac cca agc tcg aac cag aat gtc aat tcc aag gtt aat aag tac tac Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr 355 360 365	1104
agc aac cta aca aaa agt gag cgg tat agc tcc agc ggg tcc ccg gca Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala 370 375 380	1152
aac tcc ttc cac ttc aag gaa gcc tgg aag cac gca atc cag aag gcc Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala 385 390 395 400	1200
aag cac atg ccc gac ccc tgg gct gag ttc cac ctg gaa gat att gcc Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala 405 410 415	1248
acc gaa cgt gct act cga cac agg tac aac gcc gtc acc ggg gaa tgg Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp 420 425 430	1296
ctg gat gat gaa gtt ctg atc aag atg gca tct cag ccc ttc ggc cga Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg 435 440 445	1344
gga gca atg agg gag tgc ttc cgg acg aag aag ctc tcc aac ttc ttg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu 450 455 460	1392

cat gcc cag cag tgg aag ggc gcc tcc aac tac gtg gcg aag cgc tac	1440
His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr	
465 470 475 480	
atc gag ccc gta gac cgg gat gtg tac ttt gag gac gtg cgt cta cag	1488
Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln	
485 490 495	
atg gag gcc aag ctc tgg ggg gag gag tat aat cgg cac aag ccc ccc	1536
Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro	
500 505 510	
aag cag gtg gac atc atg cag atg tgc atc atc gag ctg aag gac aga	1584
Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg	
515 520 525	
ccg ggc aag ccc ctc ttc cac ctg gag cac tac atc gag ggc aag tac	1632
Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr	
530 535 540	
atc aag tac aac tcc aac tct ggc ttt gtc cgc gat gac aac atc cgc	1680
Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg	
545 550 555 560	
ctg acg ccg cag gcc ttc agc cac ttc act ttt gag cgt tcc ggc cat	1728
Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His	
565 570 575	
cag ctg ata gtg gtg gac atc cag gga gtt ggg gat ctc tac act gac	1776
Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp	
580 585 590	
cca cag atc cac acg gag acg ggc act gac ttt gga gac ggc aac cta	1824
Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu	
595 600 605	
ggg gtc cgc ggg atg gcg ctc ttc ttc tac tct cat gcc tgc aac cgg	1872
Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg	
610 615 620	
att tgc gag agc atg ggc ctt gct ccc ttt gac ctc tcg ccc cgg gag	1920
Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu	
625 630 635 640	
agg gat gca gtg aat cag aac acc aag ctg ctg caa tca gcc aag acc	1968
Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr	
645 650 655	
atc ttg aga gga aca gag gaa aaa tgt ggg agc ccc cga gta agg acc	2016
Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr	
660 665 670	
ctc tct ggg agc cgg cca ccc ctg ctc cgt ccc ctt tca gag aac tct	2064
Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser	
675 680 685	

gga gac gag aac atg agc gac gtg acc ttc gac tct ctc cct tct tcc	2112
Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser	
690 695 700	
cca tct tcg gcc aca cca cac agc cag aag cta gac cac ctc cat tgg	2160
Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp	
705 710 715 720	
cca gtc ttc agt gac ctc gat aac atg gca tcc aga gac cat gat cat	2208
Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His	
725 730 735	
cta gac aac cac cgg gag tct gag aat agt ggg gac agc gga tac ccc	2256
Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro	
740 745 750	
agt gag aag cgg ggt gag ctg gat gac cct gag ccc cga gaa cat ggc	2304
Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly	
755 760 765	
cac tca tac agt aat cgg aag tac gag tct gac gaa gac agc ctg ggc	2352
His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly	
770 775 780	
agc tct gga cgg gta tgt gta gag aag tgg aat ctc ctc aac tcc tcc	2400
Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser	
785 790 795 800	
cgc ctc cac ctg ccg agg gct tcg gcc gtg gcc ctg gaa gtg caa agg	2448
Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg	
805 810 815	
ctt aat gct ctg gac ctc gaa aag aaa atc ggg aag tcc att ttg ggg	2496
Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly	
820 825 830	
aag gtc cat ctg gcc atg gtg cgc tac cac gag ggt ggg cgc ttc tgc	2544
Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys	
835 840 845	
gag aag ggc gag gag tgg gac cag gag tcg gct gtc ttc cac ctg gag	2592
Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu	
850 855 860	
cac gca gcc aac ctg ggc gag ctg gag gcc atc gtg ggc ctg gga ctc	2640
His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu	
865 870 875 880	
atg tac tcg cag ttg cct cat cac atc cta gcc gat gtc tct ctg aag	2688
Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys	
885 890 895	
gag aca gaa gag aac aaa acc aaa gga ttt gat tac tta cta aag gcc	2736
Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala	
900 905 910	

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gct gaa gct ggc gac agg cag tcc atg atc cta gtg gcg cga gct ttt 2784
Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
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gac tct ggc cag aac ctc agc ccg gac agg tgc caa gac tgg cta gag 2832
Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
      930                      935                      940

gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag 2880
Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
      945                      950                      955                      960

ggc ggt gag tac gac gga atg cag gac gag ccc cgg tac atg atg ctg 2928
Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
      965                      970                      975

gcc agg gag gcc gag atg ctg ttc aca gga ggc tac ggg ctg gag aag 2976
Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
      980                      985                      990

gac ccg cag aga tca ggg gac ttg tat acc cag gca gca gag gca gcg 3024
Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
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atg gaa gcc atg aag ggc cga ctg gcc aac cag tac tac caa aag gct 3072
Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
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<211> 1033

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pMT-Ki-4  
(scFv)-eEF-2K ORF

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His His Ser Ser Gly His Ile Asp Asp Asp Lys His Met Lys Leu
      35          40          45
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      50          55          60
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
      65          70          75          80
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
      85          90          95
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
      100          105          110

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Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp
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	130					135					140				
Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp
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Gly	Phe	Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly
			165							170					175
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile
			180					185					190		
Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg
		195					200					205			
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser
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Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly
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Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly
			245						250					255	
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp
			260					265					270		
Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe
		275					280					285			
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Glu	Leu	Gly
	290					295					300				
Gly	Gly	Gly	Ser	Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly
305					310					315					320
Val	Asp	Gly	Gly	Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp
				325					330					335	
Gly	Asp	Ser	Asp	Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp
			340					345					350		
Asp	Pro	Ser	Ser	Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr
		355					360					365			
Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala
	370					375					380				
Asn	Ser	Phe	His	Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala
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Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala
				405					410					415	
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp
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Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg
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Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu
	450					455					460				
His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr
465					470					475					480
Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln
				485					490					495	
Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro
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Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg
		515					520					525			
Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr
	530					535					540				
Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg
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Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His
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Gln	Leu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp
			580					585					590		
Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu
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Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg
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Ile	Cys	Glu	Ser	Met	Gly	Leu	Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu
625					630					635					640
Arg	Asp	Ala	Val	Asn	Gln	Asn	Thr	Lys	Leu	Leu	Gln	Ser	Ala	Lys	Thr
				645					650					655	
Ile	Leu	Arg	Gly	Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr
			660					665					670		
Leu	Ser	Gly	Ser	Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser
		675					680					685			
Gly	Asp	Glu	Asn	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser
	690					695					700				
Pro	Ser	Ser	Ala	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp
705					710					715					720
Pro	Val	Phe	Ser	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His
				725					730					735	
Leu	Asp	Asn	His	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro
			740					745					750		
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly
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Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser
785					790					795					800
Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg
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Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly
		820						825					830		
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys
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Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu
	850					855				860					
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu
865					870					875					880
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys
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Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala
			900					905					910		
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe
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Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu
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Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu
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Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys
			980					985					990		
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala
		995					1000						1005		

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1025 1030

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
linker

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<210> 8  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: c-Myc epitope

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<210> 9  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
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domain IX of kinases

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<222> (2)  
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<220>  
<221> VARIANT  
<222> (4)..(5)  
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